CLASSIFICATION: HEAVY CONSTANT CHAINS (cont'd)

97) **MOPC173**: MOUSE IGG2A
98) **CBPC101**: MOUSE IGG2A
99) **IGA'CL**: MOUSE IGA
100) **IGA'CL'**: MOUSE IGA
101) **MOPC47A**: MOUSE IGA
102) **MOPC315**: MOUSE IGA
103) **MOPC511**: MOUSE IGA
104) **IGE'CL**: MOUSE IGE
105) **IGE'CL'**: MOUSE IGE
106) **IGE a'CL**: MOUSE IGE
107) **IGE b'CL**: MOUSE IGE
108) **IGE MEMB'CL**: MOUSE IGE MEMBRANE BOUND
112) **IR-731**: RAT IGD
113) **RAT IGG2c'CL**: RAT IGG2c
114) **RAT IGG2a'CL**: RAT IGG2a
115) **RAT IGG1'CL**: RAT IGG1
116) **RAT IGG2b'CL**: RAT IGG2b
119) **IR2'CL**: RAT IGE
121) **PM3'CL**: RABBIT MU CHAIN SECRETED (ALLOTYPE A2)
123) **RABBIT IGG**: RABBIT IGG
124) **PGAM8AB1-12,14'CL**: RABBIT IGG
125) **RABIGG**: RABBIT IGG
126) **RABIGG'CL**: RABBIT IGG
127) **P2A2'CL**: RABBIT IGG
128) **39-1A, 20B 'CL**: RABBIT IGG
129) **PA19'CL**: RABBIT IGA G-SUBCLASS
130) **CT-12**: COTTONTAIL RABBIT (SYLVILAGUS FLORIDANUS) IGG
131) **PIKA**: PIKA (OCHOTONA RUFENSIS) IGG
132) **HA-3**: HARE (LEPUS CALIFORNICUS) IGG
133) **HA-11**: HARE (LEPUS CALIFORNICUS) IGG
134) **HA-1**: HARE (LEPUS CALIFORNICUS) IGG
135) **HA-5**: HARE (LEPUS CALIFORNICUS) IGG
136) **HA-LT**: EUROPEAN HARE (LEPUF TIMIDUS) IGG
137) **SYRIAN HAMSTER IGM'CL**: SYRIAN HAMSTER LSH INBRED STRAIN
138) **GPIGG1**: GUINEA PIG IGG1
139) **GP'IGG1**: GUINEA PIG IGG1
140) **GPIGG2**: GUINEA PIG IGG2
141) **MOO**: DOG IGM
143) **SHEEP pSHC'CL**: IgG1
144) **HORSE IGG**: HORSE IGG
145) **BOVINE IGG**: BOVINE IGG
146) **GOAT IGG**: GOAT IGG
147) **CHICKEN IGM'CL**: CHICKEN IGM
149) **Ra4b'CL**: ADULT Raja erinacea (LITTLE SKATE)
150) **Ra20'CL**: ADULT Raja erinacea (LITTLE SKATE)
151) **Xenopus laevis IgY'CL**: Xenopus laevis IGM
152) **Xenopus laevis c8(II)'CL**: Xenopus laevis IGM
153) **Xenopus laevis c14(II)'CL**: Xenopus laevis IGM
154) **Xenopus laevis c35'CL**: Xenopus laevis IGM
155) **Xenopus laevis c40(II)'CL**: Xenopus laevis IGM
156) **Xenopus laevis J2(I)'CL**: Xenopus laevis IGM
157) **Xenopus laevis J4(III)'CL**: Xenopus laevis IGM
158) **Xenopus laevis J6(I)'CL**: Xenopus laevis IGM
159) **Xenopus laevis J12(IV)'CL**: Xenopus laevis IGM

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36) **HUMAN IGG1'CL**: ELLISON,J.W.,BERSON,B.J. & HOOD,L.E. (1982) NUC.ACIDS RES.,10,4071-4079; KRAWINKEL,U. & RABBITTS,T.H. (1982) EMBO J.,1,403-407; TAKAHASHI,N.,UEDA,S.,OBATA,M.,NIKAIDO,T.,NAKAI,S. & HONJO,T. (1982) CELL,29,671-679.

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81) **IGG1'CL**: HONJO,T.,OBATA,M.,YAMAWAKI-KATAOKA,Y.,KATAOKA,T.,KAWAKAMI,T.,TAKAHASHI,N. & MANO,Y. (1979) CELL,18,559-568. (CHECKED BY AUTHOR 11/29/82); SAKANO,H.,ROGERS,J.H.,HUPPI,K.,BRACK,C.,TRAUNECKER,A.,MAKI,R.,WALL,R. & TONEGAWA, S. (1979) NATURE,277,627-633; OBATA,M.,YAMAWAKI-KATAOKA,Y.,TAKAHASHI,N.,KATAOKA,T.,SHIMIZU,A.,MANO,Y.,SEIDMAN, J.G.,PETERLIN,B.M.,LEDER,P. & HONJO,T. (1980) GENE,9,87-97.

82) **IGG1 MEMB'CL**: ROGERS,J.,CHOI,E.,SOUZA,L.,CARTER,C.,WORD,C.,KUEHL,M.,EISENBERG,D. & WALL,R. (1981) CELL,26,19-27. (CHECKED BY AUTHOR 12/07/81); TYLER,B.M.,COWMAN,A.F.,GERONDAKIS,S.D.,ADAMS,J.M. & BERNARD,O. (1982) PROC.NAT.ACAD.SCI.USA,79,2008-2012; YAMAWAKI-KATAOKA,Y.,NAKAI,S.,MIYATA,T. & HONJO,T. (1982) PROC.NAT.ACAD.SCI.USA,79,2623-2627.

83) **MOPC21**: ADETUGBO,K.,MILSTEIN,C. & SECHER,D.S. (1977) NATURE,265,299-304; ADETUGBO,K. (1978) J.BIOL.CHEM.,253,6068-6075.

84) **IF2'CL**: DUNNICK,W.,RABBITTS,T.H. & MILSTEIN,C. (1980) NUC.ACIDS RES.,8,1475-1484. (CHECKED BY AUTHOR 11/30/82)

85) **ICR 11.19.3**: BIRSHTEIN,B.K.,CAMPBELL,R. & GREENBERG,M.L. (1980) BIOCHEMISTRY,19,1730-1737. (CHECKED BY AUTHOR 11/25/81)

86) **IGG2B(A)'CL**: TUCKER,P.W.,MARCU,K.B.,NEWELL,N.,RICHARDS,J. & BLATTNER,F.R. (1979) SCIENCE,206,1303-1306. (CHECKED BY AUTHOR 12/06/82 WHO CORRECTED RESIDUES AT POSITIONS 146, 203, 213 AND 218 AS SHOWN)

87) **IGG2B(A)'CL'**: YAMAWAKI-KATAOKA,Y.,KATAOKA,T.,TAKAHASHI,N.,OBATA,M. & HONJO,T. (1980) NATURE,283,786-789. (CHECKED BY AUTHOR 07/06/81)

88) **IGG2B(B)'CL**: OLLO,R. & ROUGEON,F. (1982) NATURE,296,761-763.

89) **IGG2B MEMB'CL**: ROGERS,J.,CHOI,E.,SOUZA,L.,CARTER,C.,WORD,C.,KUEHL,M.,EISENBERG,D. & WALL,R. (1981) CELL,26,19-27. (CHECKED BY AUTHOR 12/07/81); TYLER,B.M.,COWMAN,A.F.,GERONDAKIS,S.D.,ADAMS,J.M. & BERNARD,O. (1982) PROC.NAT.ACAD.SCI.USA,79,2008-2012; YAMAWAKI-KATAOKA,Y.,NAKAI,S.,MIYATA,T. & HONJO,T. (1982) PROC.NAT.ACAD.SCI.USA,79,2623-2627.

90) **MPC11**: FRANCUS,T. & BIRSHTEIN,B.K. (1978) BIOCHEMISTRY,17,4324-4331; BIRSHTEIN,B.K.,CAMPBELL,R. & GREENBERG,M.L. (1980) BIOCHEMISTRY,19,1730-1737. (CHECKED BY AUTHOR 07/08/80)

91) **10.1**: BRANDT,C.R.,MORRISON,S.L.,BIRSHTEIN,B.K. & MILCAREK,C. (1984) MOL.CELL.BIOL.,4,1270-1277.

92) **IGG2A(A)'CL**: SIKORAV,J.L.,AUFFRAY,C. & ROUGEON,F. (1980) NUC.ACIDS RES.,8,3143-3155; OLLO,R.,AUFFRAY,C.,MORCHAMPS,C. & ROUGEON,F. (1981) PROC.NAT.ACAD.SCI.USA,78,2442-2446; YAMAWAKI-KATAOKA,Y.,MIYATA,T. & HONJO,T. (1981) NUC.ACIDS RES.,9,1365-1381. (CHECKED BY AUTHOR (HONJO) 11/29/82); OLLO,R. & ROUGEON,F. (1983) CELL,32,515-523.

93) **17/9'CL**: SCHULZE-GAHMEN,U.,RINI,J.M.,AREVALO,J.,STURA,E.,KENTEN,J.H. & WILSON,I.A. (1988) J.BIOL.CHEM.,263,17100-17106.

94) **IGG2A(B)'CL**: SCHREIER,P.H.,BOTHWELL,A.L.M.,MUELLER-HILL,B. & BALTIMORE,D. (1981) PROC.NAT.ACAD.SCI.USA,78,4495-4499. (CHECKED BY AUTHOR 08/03/81)

95) **IGG2A(B)'CL'**: OLLO,R. & ROUGEON,F. (1983) CELL,32,515-523.

96) **IGG2A MEMB'CL**: ISHIDA,N.,UEDA,S.,HAYASHIDA,H.,MIYATA,T. & HONJO,T. (1982) EMBO J.,1,1117-1123; YAMAWAKI-KATAOKA,Y., NAKAI,S.,MIYATA,T. & HONJO,T. (1982) PROC.NAT.ACAD.SCI.USA,79,2623-2627.

97) **MOPC173**: FOUGEREAU,M.,BOURGOIS,A.,DE PREVAL,C.,ROCCA-SERRA,J. & SCHIFF,C. (1976) ANNALES D'IMMUNOLOGIE,127C,607-631. (CHECKED BY AUTHOR 01/11/83)

98) **CBPC101**: DOGNIN,M.J.,LAUWEREYS,M. & STROSBERG,A.D. (1981) PROC.NAT.ACAD.SCI.USA,78,4031-4035. (CHECKED BY AUTHOR 01/04/83)

99) **IGA'CL**: AUFFRAY,C.,NAGEOTTE,R.SIKORAV,J-L.,HEIDMANN,O. & ROUGEON,F. (1981) GENE,13,365-374.

100) **IGA'CL'**: TUCKER,P.W.,SLIGHTOM,J.L. & BLATTNER,F.R. (1981) PROC.NAT.ACAD.SCI.USA,78,7684-7688. (CHECKED BY AUTHOR 12/06/82)

101) **MOPC47A**: ROBINSON,E.A. & APPELLA,E. (1977) PROC.NAT.ACAD.SCI.USA,74,2465-2469; ROBINSON,E.A. & APPELLA,E. (1979) J.BIOL.CHEM.,254,11418-11430. (CHECKED BY AUTHOR 01/11/83)

102) **MOPC315**: FRANCIS,S.H.,LESLIE,R.G.Q.,HOOD,L. & EISEN,H.N. (1974) PROC.NAT.ACAD.SCI.USA,71,1123-1127; ROBINSON,E.A. & APPELLA,E. (1977) PROC.NAT.ACAD.SCI.USA,74,2465-2469.

REFERENCE: HEAVY CONSTANT CHAINS (cont'd)

103) **MOPC511**: FRANCIS,S.H.,LESLIE,R.G.Q.,HOOD,L. & EISEN,H.N. (1974) PROC.NAT.ACAD.SCI.USA,71,1123-1127; ROBINSON,E.A. & APPELLA,E. (1977) PROC.NAT.ACAD.SCI.USA,74,2465-2469; ROBINSON,E.A. & APPELLA,E. (1980) PROC.NAT.ACAD.SCI.USA,77, 4909-4913. (CHECKED BY AUTHOR 10/17/80 WHO CORRECTED RESIDUE AT POSITION 384 FROM GLY TO GLU.)

104) **IGE'CL**: NISHIDA,Y.,KATAOKA,T.,ISHIDA,N.,NAKAI,S.,KISHIMOTO,T.,BOTTCHER,I. & HONJO,T. (1981) PROC.NAT.ACAD.SCI.USA,78, 1581-1585; ISHIDA,N.,UEDA,S.,HAYASHIDA,H.,MIYATA,T. & HONJO,T. (1982) EMBO J.,1,1117-1123.

105) **IGE'CL'**: LIU,F.-T.,ALBRANDT,K.,SUTCLIFFE,J.G. & KATZ,D.H. (1982) PROC.NAT.ACAD.SCI.USA,79,7852-7856. (CHECKED BY AUTHOR 06/03/83)

106) **IGE a'CL**: SHINKAI,Y.,NAKAUCHI,H.,HONJO,T. & OKUMURA,K. (1988) IMMUNOGENET.,27,288-292.

107) **IGE b'CL**: SHINKAI,Y.,NAKAUCHI,H.,HONJO,T. & OKUMURA,K. (1988) IMMUNOGENET.,27,288-292.

108) **IGE MEMB'CL**: ISHIDA,N.,UEDA,S.,HAYASHIDA,H.,MIYATA,T. & HONJO,T. (1982) EMBO J.,1,1117-1123.

109) **IGA MEMB'CL**: WORD,C.J.,MUSHINSKI,J.F.,TUCKER,P.W. (1983) EMBO J.,2,887-898.

110) **RAT IGM'CL**: BRUGGEMANN,M.,FREE,J.,DIAMOND,A.,HOWARD,J.,COBBOLD,S. & WALDMANN,H. (1986) PROC.NATL.ACAD.SCI.USA,83, 6075-6079.

111) **RAT IGD'CL**: SIRE,J.,AUFFRAY,C. & JORDAN,B.R. (1982) GENE,20,377-386.

112) **IR-731**: ALCARAZ,G.,BOURGOIS,A.,MOULIN,A.,BAZIN,H. & FOUGEREAU,M. (1980) ANN.IMMUNOL.(INST.PASTEUR),131C,363-388. (CHECKED BY AUTHOR 01/11/83)

113) **RAT IGG2c'CL**: BRUGGEMANN,M.,DELMASTRO-GALFRE,P.,WALDMANN,H. & CALABI,F. (1988) EUR.J.IMMUNOL.,18,317-319.

114) **RAT IGG2a'CL**: BRUGGEMANN,M. (1988) GENE,74,473-482.

115) **RAT IGG1'CL**: BRUGGEMANN,M. (1988) GENE,74,473-482.

116) **RAT IGG2b'CL**: BRUGGEMANN,M. (1988) GENE,74,473-482.

117) **RAT IGA'CL**: BRUGGEMANN,M.,FREE,J.,DIAMOND,A.,HOWARD,J.,COBBOLD,S. & WALDMANN,H. (1986) PROC.NATL.ACAD.SCI.USA,83, 6075-6079.

118) **RAT IGE 'CL**: STEEN,M.L.,HELLMAN,L. & PETTERSSON,U. (1984) J.MOL.BIOL.,177,19-32.

119) **IR2'CL**: HELLMAN,L.,PETTERSSON,U. & BENNICH,H. (1982) PROC.NAT.ACAD.SCI.USA,79,1264-1268; HELLMAN,L,PETTERSSON,U., ENGSTROM,A.,KARLSSON,T. & BENNICH,H. (1982) NUC.ACIDS RES.,10,6041-6049.

120) **IR-162'CL**: KINDSVOGEL,W.R.,REDDY,E.P.,MOORE,J.M. & FAUST,C.H.,JR. (1982) DNA 1,335-343.

121) **PM3'CL**: BERNSTEIN,K.E.,ALEXANDER,C.B.,REDDY,E.P. & MAGE,R.G. (1984) J.IMMUNOL.,132,490-495.

122) **PME5'CL**: BERNSTEIN,K.E.,ALEXANDER,C.B.,REDDY,E.P. & MAGE,R.G. (1984) J.IMMUNOL.,132,490-495.

123) **RABBIT IGG**: PRATT,D.M. & MOLE,L.E. (1975) BIOCHEM.J.,151,337-349.

124) **PGAMMAB1-12,14'CL**: BERNSTEIN,K.E.,ALEXANDER,C.B. & MAGE,R.G. (1983) IMMUNOGENETICS,18,387-397.

125) **RABIGG**: FRUCHTER,R.G.,JACKSON,S.A.,MOLE,L.E. & PORTER,R.R. (1970) BIOCHEM.J.,116,249-259. (CHECKED BY AUTHOR 12/10/82); HILL,R.L.,LEBOVITZ,G.E.,FELLOWS,R.E.,JR. & DELANEY,R. (1967) IN GAMMA GLOBULINS,NOBEL SYMP. 3, KILLANDER,J.,ED.,PP.109-127,ALMQUIST AND WIKSELL,STOCKHOLM.

126) **RABIGG'CL**: HEIDMANN,O. & ROUGEON,F. (1982) NUC.ACIDS RES.,10,1535-1545.

127) **P2A2'CL**: MARTENS,C.L.,MOORE,K.W.,STEINMETZ,M.,HOOD,L. & KNIGHT,K.L. (1982) PROC.NAT.ACAD.SCI.USA,79,6018-6022.

128) **39-1A, 20B 'CL**: MARTENS,C.L.,CURRIER,S.J. & KNIGHT,K.L. (1984) J. IMMUNOL.,133,1022-1027.

129) **PA19'CL**: KNIGHT,K.L.,MARTENS,C.L.,STOKLOSA,C.M. & SCHNEIDERMAN,R.D. (1984) NUC.ACIDS RES.,12,1657-1669.

130) **CT-12**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80); TEHERANI,J.,CAPRA,J.D. & MANDY,W.J. (1982) MOL.IMMUNOL.,19,841-846.

131) **PIKA**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80); TEHERANI,J.,CAPRA,J.D. & MANDY,W.J. (1982) MOL.IMMUNOL.,19,841-846.

132) **HA-3**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80); TEHERANI,J.,CAPRA,J.D. & MANDY,W.J. (1982) MOL.IMMUNOL.,19,841-846.

133) **HA-11**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80)

134) **HA-1**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80); TEHERANI,J.,CAPRA,J.D. & MANDY,W.J. (1982) MOL.IMMUNOL.,19,841-846.

135) **HA-5**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80)

136) **HA-LT**: TEHERANI,J.,CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695. (CHECKED BY AUTHOR 07/31/80); TEHERANI,J.,CAPRA,J.D. & MANDY,W.J. (1982) MOL.IMMUNOL.,19,841-846.

137) **SYRIAN HAMSTER IGM'CL**: MCGUIRE,K.L.,DUNCAN,W.R. & TUCKER,P.W. (1985) NUC.ACIDS RES.,13,5611-5628. (FROM EMBL 03/27/87)

138) **GPIGG1**: CEBRA,J.,BRUNHOUSE,R.,CORDLE,C.,DAISS,J.,FECHHEIMER,M.,RICARDO,M.,THUNBERG,A. & WOLFE,P.B. (1977) PROG.IMMUNOL., 3,269-277. (CHECKED BY AUTHOR 08/08/79); BRUNHOUSE,R. & CEBRA,J.J. (1979) MOL.IMMUNOL.,16,907-917.

139) **GP'IGG1**: MELAMED,M.D. (1976) IMMUNOCHEM.,13,271-279.

140) **GPIGG2**: TRISCHMANN,T.M. & CEBRA,J.J. (1974) BIOCHEMISTRY,13,4804-4811; CEBRA,J.,BRUNHOUSE,R.,CORDLE,C.,DAISS,J., FECHHEIMER,M.,RICARDO,M.,THUNBERG,A. & WOLFE,P.B. (1977) PROG.IMMUNOL.,3,269-277. (CHECKED BY AUTHOR 08/08/79); BRUNHOUSE,R. & CEBRA,J.J. (1979) MOL.IMMUNOL.,16,907-917.

141) **MOO**: WASSERMAN,R.L. & CAPRA,J.D. (1978) SCIENCE,200,1159-1161; MCCUMBER,L.J. & CAPRA,J.D. (1979) MOL.IMMUNOL.,16, 565-570. (CHECKED BY AUTHOR 08/01/79)

142) **PIG IGG**: METZGER,J.J. & PERY,P. (1973) BIOCHEM.BIOPHYS.RES.COMMUN.,55,253-259. (CHECKED BY AUTHOR 07/13/83)

143) **SHEEP pSEC'CL**: FOLEY,R.C. & BEH,K.J. (1989) J.IMMUNOL.,142,708-711.

144) **HORSE IGG**: WEIR,R.C.,PORTER,R.R. & GIVOL,D. (1966) NATURE,212,205-206. (CHECKED BY AUTHOR 08/10/79)

145) **BOVINE IGG**: INOUVE,H. & GIVOL,D. (1967) ISRAEL J.CHEM.,5,106P. (CHECKED BY AUTHOR 08/10/79)

146) **GOAT IGG**: STRAUSBAUCH,P.H.,HURWITZ,E. & GIVOL,D. (1971) BIOCHEMISTRY,10,2231-2237. (CHECKED BY AUTHOR 07/26/79)

147) **CHICKEN IGM'CL**: DAHAN,A.,REYNAUD,C.A. & WEILL,J.C. (1983) NUC.ACIDS RES.,11,5381-5389.

148) **Elops VH'CL**: AMEMIYA,C.T. & LITMAN,G.W. (1990) PROC.NATL.ACAD.SCI.USA,87,811-815.

149) **Re4b'CL**: HARDING,F.A.,AMEMIYA,C.T.,LITMAN,R.T.,COHEN,N. & LITMAN,G.W. (1990) NUCL.ACIDS RES.,18,6369-6376.

150) **Re20'CL**: HARDING,F.A.,AMEMIYA,C.T.,LITMAN,R.T.,COHEN,N. & LITMAN,G.W. (1990) NUCL.ACIDS RES.,18,6369-6376.

151) **Xenopus laevis IgY'CL**: AMEMIYA,C.T.,HAIRE,R.N. & LITMAN,G.W. (1989) NUCL.ACIDS RES.,17,5388.

152) **Xenopus laevis c8(II)'CL**: SCHWAGER,J.,MIKORYAK,C.A. & STEINER,L.A. (1988) PROC.NATL.ACAD.SCI.USA,85,85,2245-2249; SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

153) **Xenopus laevis c14(II)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

154) **Xenopus laevis c35'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

155) **Xenopus laevis c40(II)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

156) **Xenopus laevis J2(I)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

157) **Xenopus laevis J4(III)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

158) **Xenopus laevis J6(I)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

159) **Xenopus laevis J12(IV)'CL**: SCHWAGER,J.,GROSSBERGER,D. & DU PASQUIER,L. (1988) EMBO J.,7,2409-2415.

GENERAL NOTES: HEAVY CONSTANT CHAINS

\# CH1, HINGE, CH2, CH3 AND CH4 DOMAINS ARE TABULATED TO CONFORM TO THEIR CODING NUCLEOTIDE SEQUENCES RELATIVE TO INTERVENING SEQUENCES ESTABLISHED BY SAKANO,H.,ROGER,J.H.,HUPPI,K.,BRACK,C.,TRAUNECKER,A.,MAKI,R.,WALL,R. & TONEGAWA,S. (1979) NATURE,277,627-633. A MEMBRANE DOMAIN IS LISTED SEPARATEDLY TO INCLUDE PART OF THE C-TERMINAL PORTION OF MEMBRANE BOUND IMMUNOGLOBULINS. IF IT IS DESIRED TO ALIGN THE LIGHT CHAIN WITH THE HEAVY CHAIN DOMAINS FOR HOMOLOGY, THE SEQUENTIAL NUMBERING IN THE FIRST COLUMN SHOULD BE USED: RESIDUES 108 TO 215 FOR CL; 114 TO 223 IN CH1 PLUS THE FIRST PART OF HINGE (224 TO 241), THE END OF HINGE (242 AND 243) AND THE FIRST TWO RESIDUES OF CH2 (244 AND 245); 246 THROUGH 361 OF CH2; 362 THROUGH 496 OF CH3; AND 497 THROUGH 628 OF CH4. GAPS IN THE SEQUENTIAL NUMBERING ARE USED FOR ALIGNMENT.

\# DISULFIDE BONDS ARE LOCATED AT THE FOLLOWING POSITIONS IF CYS IS PRESENT:

INTRACHAIN:	142-208,274-340,249-312,390-456,524-587.
HL-INTERCHAIN:	127 OR 128,198 OR 225,230,235.
HH-INTERCHAIN:	232,233,237,238,239,240,241A,G,M,P,V,BB,EE,KK,QQ,242,248,261,314.
INTERSUBUNIT:	328,444.
TO J-CHAIN:	495,627.

IDENTIFICATIONS OF SOME OF THESE DISULFIDE BONDS ARE NOT ABSOLUTELY CERTAIN.

\# THERE WOULD APPEAR TO BE POLYMORPHISM AMONG GAL, OU, SCO AND BOT/CO MU-CHAINS AS FOLLOWS:

GAL	SER-334, VAL-358

SPECIFIC NOTES: HEAVY CONSTANT CHAINS

1) **HUMAN IGM'CL:** THE AMINO ACID SEQUENCE WAS OBTAINED BY TRANSLATING A CLONE OF HUMAN FETAL LIVER DNA.

5) **BOT:** FROM A CASE OF IGM HEAVY CHAIN DISEASE. THE AMINO ACID RESIDUES AT POSITIONS 451 TO 476, 519 TO 544 AND 608 TO 628 ARE IDENTICAL TO THAT OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN DNA CONTAINING THE IGM GENE (TAKAHASHI,N.,NAKAI,S. & HONJO,T. (1980) NUCL.ACIDS RES.,8,5983-5991).

7) **GLI:** IT HAS NO VARIABLE REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE.

9) **WAH:** THE SEQUENCES OF WAH AND NIG-65 ARE IDENTICAL FOR POSITIONS 241 PP TO 485 WHERE BOTH SEQUENCES ARE DETERMINED. FOR WAH, THERE ARE FOUR OR FIVE N-ACETYL-D-GALACTOSAMINE OLIGOSACCHARIDES ATTACHED TO SER AT POSITION 234, AND THR AT POSITIONS 241 J, 241 K, AND 241 O AND/OR 241 P. FOR NIG-65, THERE ARE THREE N-ACETYL-D-GLUCOSAMINE OLIGOSACCHARIDES ATTACHED TO ASN AT POSITIONS 314, 414 AND 468.

10) **NIG-65:** THE SEQUENCES OF WAH AND NIG-65 ARE IDENTICAL FOR POSITIONS 241 PP TO 485 WHERE BOTH SEQUENCES ARE DETERMINED. FOR WAH, THERE ARE FOUR OR FIVE N-ACETYL-D-GALACTOSAMINE OLIGOSACCHARIDES ATTACHED TO SER AT POSITION 234, AND THR AT POSITIONS 241 J, 241 K, AND 241 O AND/OR 241 P. FOR NIG-65, THERE ARE THREE N-ACETYL-D-GLUCOSAMINE OLIGOSACCHARIDES ATTACHED TO ASN AT POSITIONS 314, 414 AND 468.

11) **ERI:** THERE ARE THREE AMINO ACID RESIDUES BETWEEN POSITION 140 AND POSITION 142; THEY ARE ALA, VAL AND ALA. THE AUTHOR HAS RECENTLY INDICATED THAT THERE IS ONLY ONE AMINO ACID RESIDUE THERE AND IT IS ALA.

14) **HUMAN IGG3'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF THREE CLONES OF HUMAN GENOMIC DNA. THERE ARE FOUR EXONS: POSITIONS 216 TO 241B, 241C TO 241Q, 241R TO 241FF, AND 241GG TO 243.

15) **OMM'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CELL LINE CDNA. FROM A CASE OF HEAVY CHAIN DISEASE.

16) **HER:** THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.

17) **FRO:** THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.

18) **JON:** THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.

19) **WIS:** FROM A CASE OF HEAVY CHAIN DISEASE.

20) **SPA:** FROM A CASE OF HEAVY CHAIN DISEASE.

21) **ZUC:** FROM A CASE OF HEAVY CHAIN DISEASE.

22) **ZUC':** OBTAINED FROM THE SAME PATIENT AS ZUC, AND EXISTED IN A MONOMER FORM.

23) **KUP:** THE SEQUENCES OF KUP AND BRU ARE IDENTICAL.

24) **BRU:** THE SEQUENCES OF KUP AND BRU ARE IDENTICAL.

26) **CHA:** IT HAS NO VARIABLE REGION AND NO CH1 REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE. AMINO ACID RESIDUES FOUND AT POSITION 224 ARE THR AND SER.

29) **NIE:** IN EARLIER EDITIONS, THE AMINO ACID RESIDUES AT POSITIONS 238, 285, 300 AND 331 LISTED BY US WERE INCORRECT.

30) **CRA:** FROM A CASE OF HEAVY CHAIN DISEASE.

31) **VAU:** FROM A CASE OF HEAVY CHAIN DISEASE.

32) **LEB:** FROM A CASE OF HEAVY CHAIN DISEASE.

33) **EST:** IT HAS NO VARIABLE REGION AND NO CH1 REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE.

34) **YOK:** THE GLY AT POSITION 462 IN IGG1 CHAIN IS CONSIDERED TO BE ASSOCIATED WITH THE GM(2) ALLOTYPE (COOK,E. & STEINBERG, A.G. (1979) MOL.IMMUNOL.,16,555-558).

36) **HUMAN IGG1'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A HUMAN FETAL LIVER DNA.

41) **BUR:** THE AMINO ACID RESIDUES AT POSITIONS 262,263,269,304,310,333,430,431,447,461 AND 490 HAVE RECENTLY BEEN REVISED BY THE AUTHORS (PUTNAM,F.W.,LIU,Y.S.V. & LOW,T.L.K. (1979) J.BIOL.CHEM.,254,2865-2874.) FROM GLN,ASP,GLU,GLN,ASP, ASN,GLN,GLY,ASP,GLU AND GLU TO GLX,ASX,GLX,GLX,ASX,ASX,GLX,GLN,ASX,GLX AND GLN RESPECTIVELY.

43) **CAR:** THE SEQUENCE WAS OBTAINED AFTER DIGESTION WITH PROTEASES. PROTEASES FROM S. SANGUIS AND S. PNEUMONIAE CLEAVED BETWEEN POSITIONS 241C AND 241D, AND THAT FROM H. INFLUENZAE BETWEEN POSITIONS 241G AND 241H.

47) **HUMAN IGG'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA. THIS GENE IS NOT EXPRESSED DUE TO THE LACK OF A SWITCH REGION, AND IS THUS DESIGNATED AS PSEUDO-GAMMA IGHGP. IT IS LOCATED BETWEEN IGGA1 AND IGG2.

48) **HUMAN IGG2'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC DNA.

53) **HUMAN IGG4'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC DNA.

55) **HUMAN IGE'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCES OF CLONES OF HUMAN GENOMIC DNA FROM FETAL LIVER (NISHIDA,Y.,MIKI,T., HISAJIMA,H. & HONJO,T. (1982) PROC.NAT.ACAD.SCI.USA,79,3833-3837) AND PLACENTA (MAX,E.E.,BATTEY,J.,NEY,R.,KIRSCH,I.R. & LEDER,P. (1982) CELL,29,691-699), AND FROM A HUMAN IGE-PRODUCING MYELOMA (266B1 (FLANAGAN,J.G. & RABBITTS,T.H. (1982) EMBO J.,1,655-660). ALL THREE SEQUENCES HAVE LEU AT POSITION 272 AND AN EXTRA LEU AT POSITION 273 NOT REPORTED BY AMINO ACID SEQUENCING IN IGE MYELOMA ND. MAX ET AL. AND FLANAGAN & RABBITTS CARRIED OUT COMPLETE NUCLEOTIDE SEQUENCES AND NISHIDA ET AL. PARTIAL SEQUENCES. EXCEPT FOR RESIDUE 538 WHICH IS REPORTED AS LEU BY MAX ET AL. AND AS TRP BY FLANAGAN & RABBITTS, ALL AMINO ACID RESIDUES ARE IDENTICAL.

56) **HUMAN IGE'CL':** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CDNA.

66) **IGM'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF NEWBORN MOUSE DNA. THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH1 AND CH2, CH2 AND CH3, AND CH3 AND CH4 ARE 110, 279, AND 107 BASE-PAIRS RESPECTIVELY. (MATTHYSSENS,G. & RABBITTS,T.H. ((1980) NUCL.ACIDS RES.,8,703-713) HAVE ALSO OBTAINED AMINO ACID RESIDUES 583 TO 628 FROM THE NUCLEOTIDE SEQUENCES. CALAME,K.,ROGERS,J.,EARLY,P.,DAVIS,M.,EIVANT,D., WALL,R. & HOOD,L. (1980) NATURE,284,452-455) BY NUCLEOTIDE SEQUENCING OF AMINO ACIDS 320 TO 343 AND 593 TO 628 FOUND ACT CODING FOR THR AT POSITION 328.

67) **IGM'CL':** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA. A SINGLE AMINO ACID SUBSTITUTION AT POSITION 436 FROM SER TO ASN RESULTS IN A MUTANT PROTEIN WHICH IS DEFECTIVE IN INITIATING COMPLEMENT-DEPENDENT CYTOLYSIS. (SHULMAN,M.J.,PENNELL,N.,COLLINS,C. &HOZUMI,N. (1986) PROC.NATL.ACAD.SCI.USA,83,7678-7682.)

69) **MUTANT 102'CL:** IT LACKS CODONS 601 TO 614, SO THAT PREDOMINANTLY MONOMERIC IgM WAS PRODUCED BY THIS CELL LINE.

71) **MOPC104E MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CDNA CLONE.

72) **HPC76'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CDNA CLONE.

75) **IGD'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA.

76) **IGD SECR'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.

77) **IGD MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.

81) **IGG1'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF NEWBORN MOUSE DNA. THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH1 AND HINGE, HINGE AND CH2, AND CH2 AND CH3 ARE 356, 98, AND 121 BASE-PAIRS RESPECTIVELY. HONJO ET AL. HAVE DETERMINED THE ENTIRE SEQUENCE, WHILE SAKANO ET AL. HAVE DETERMINED RESIDUES 114 TO 128, 202 TO 268, AND 335 TO 376. THEY ARE IDENTICAL AT CORRESPONDING POSITIONS.

82) **IGG1 MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

84) **IF2'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA FROM CELL LINE IF2. THE CH1 REGION IS DELETED.

86) **IGG2B(A)'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA. THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH1 AND HINGE, HINGE AND CH2, AND CH2 AND CH3 ARE 316, 108, AND 112 BASE-PAIRS RESPECTIVELY.

87) **IGG2B(A)'CL':** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA. THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH1 AND HINGE, HINGE AND CH2, AND CH2 AND CH3 ARE 316, 107, AND 112 BASE-PAIRS RESPECTIVELY.

88) **IGG2B(B)'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA. THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH1 AND HINGE, HINGE AND CH2, AND CH2 AND CH3 ARE 317, 108, AND 113 BASE-PAIRS RESPECTIVELY.

89) **IGG2B MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

90) **MPC11:** THE AMINO ACID RESIDUES AT POSITION 363 WERE FOUND TO BE ILE AND LEU.

91) **10.1:** THIS PROTEIN IS OBTAINED FROM A MUTANT OF MPC11 WITH A DELETION OF 99 NUCLEOTIDES INCLUDING THE 3' END OF THE CH1 EXON, GIVING RISE TO A DELETION OF THE ENTIRE CH1 REGION OF THE PROTEIN.

92) **IGG2A(A)'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

93) **17/9'CL:** THE Fab FRAGMENT OF 17/9 (IGG2a-KAPPA) HAS BEEN CRYSTALLIZED.

94) **IGG2A(B)'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

95) **IGG2A MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

96) **IGA'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

97) **IGA'CL':** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF BALB/C MOUSE LIVER DNA. THE HINGE SEGMENT OF THE HINGE REGION IS NOT ON A SEPARATE EXON. THE FIRST THREE AMINO ACID RESIDUES BELONG TO THE CH1 EXON, AND THE REMAINING NINE AMINO ACID RESIDUES BELONG TO THE CH2 EXON. THEY HAVE BEEN PLACED IN THE HINGE DOMAIN SINCE THEY ALIGN PERFECTLY WITH OTHER IGAS.

100) **MOPC511:** CARBOHYDRATES ARE ATTACHED AT POSITIONS 154 AND 483.

101) **IGE'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA FROM AN IGE-PRODUCING HYBRIDOMA.

102) **IGE a'CL:** FROM BALB/c MOUSE LIVER DNA.

103) **IGE b'CL:** FROM BIO.A MOUSE LIVER DNA.

104) **IGE MEMB'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF DNA FROM NEWBORN MOUSE.

110) **RAT IGD'CL:** THE AMINO ACID SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT CDNA.

111) **IR2'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT CDNA.

112) **IR-162'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT DNA.

114) **PGAMMAB1-12.14'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RABBIT CDNA.

115) **RABIGG:** THE AMINO ACID SEQUENCE FOR POSITIONS 266 TO 275 AND 321 TO 336 WAS ALSO CONFIRMED BY OTHERS (TEHERANI,J., CAPRA,J.D.,AGGARWAL,S. & MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695.).

117) **P2A2'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RABBIT CDNA.

SPECIFIC NOTES: HEAVY CONS

143) **SHEEP pSEC'CL:** TRANSLATED

144) **HORSE IGG:** AS COMPARED WI

147) **CHICKEN IGM'CL:** THE AMINC

148) **Elops VH'CL:** FROM Elops sa

152) **Xenopus laevis c8(II)'CL:**

153) **Xenopus laevis c14(II)'CL:**

* THE FOLLOWING WERE EQUALLY A

AT POSITION	
113D	(ILE
113E	
137	
158	
224	
241B	
243I	
281	
307	
326	
343	
351A	(
403	
452	
496C	
511	
532	
545	
580B	
637	
657	
662	(
663	

SPECIFIC NOTES: HEAVY CONSTANT CHAINS (cont'd)

143) **SHEEP pSHC'CL**: TRANSLATED FROM cDNA OF SHEEP LYMPHOCYTES
144) **HORSE IGG**: AS COMPARED WITH HORSE IGG, THE HORSE T PROTEIN HAD VAL AT POSITION 463, GLU AT 464, AND HIS AT 474.
147) **CHICKEN IGM'CL**: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE SEQUENCE OF A CLONE OF CHICKEN CDNA.
148) **Elops VH'CL**: FROM Elops saurus (LADYFISH).
152) **Xenopus laevis c8(II)'CL**: ALSO KNOWN AS XIg8'CL.
153) **Xenopus laevis c14(II)'CL**: ALSO KNOWN AS XIg14'CL.

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
113D	(ILE,GLN), (ILE,GLU)
113E	(CYS,SER)
137	(THR,SER)
158	(LYS,ASN)
224	(ARG,GLU)
241B	(PRO,CYS)
243I	(ALA,SER)
281	(PRO,GLU)
307	(PRO,LYS)
326	(PRO,THR)
343	(THR,ASN)
351A	(LEU,THR,ASN)
403	(THR,ASN)
452	(ASP,ASN)
496C	(PRO,ALA)
511	(ARG,GLU)
532	(ALA,GLU)
545	(PRO,LEU)
580B	(MET,ASP)
637	(LEU,VAL)
657	(GLU,GLN)
662	(ILE,VAL,ALA)
663	(ILE,SER)